# Az R adatelemzési nyelv alapjai I.

Egészségügyi informatika és biostatisztika

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### What R is and what it is not

#### • R is

- a programming language
- a statistical package
- an interpreter
- Open Source

#### • R is not

- SPSS, Statistica, etc.
- a collection of "black boxes"
- a spreadsheet software package
- commercially supported

### What R is

- data handling and storage: numeric, textual
- matrix algebra
- regular expressions
- high-level data analytic and statistical functions
- classes ("OO")
- graphics
- programming language: loops, branching, functions

### What R is not

- has no click-point user interfaces
- language interpreter can be very slow, but allows to call own C/C++ code
- no spreadsheet view of data, but connects to Excel/MsOffice
- no professional /commercial support

### R and statistics

 Packaging: a crucial infrastructure to efficiently produce, load and keep consistent software libraries from (many) different sources / authors

 Statistics: most packages deal with statistics and data analysis

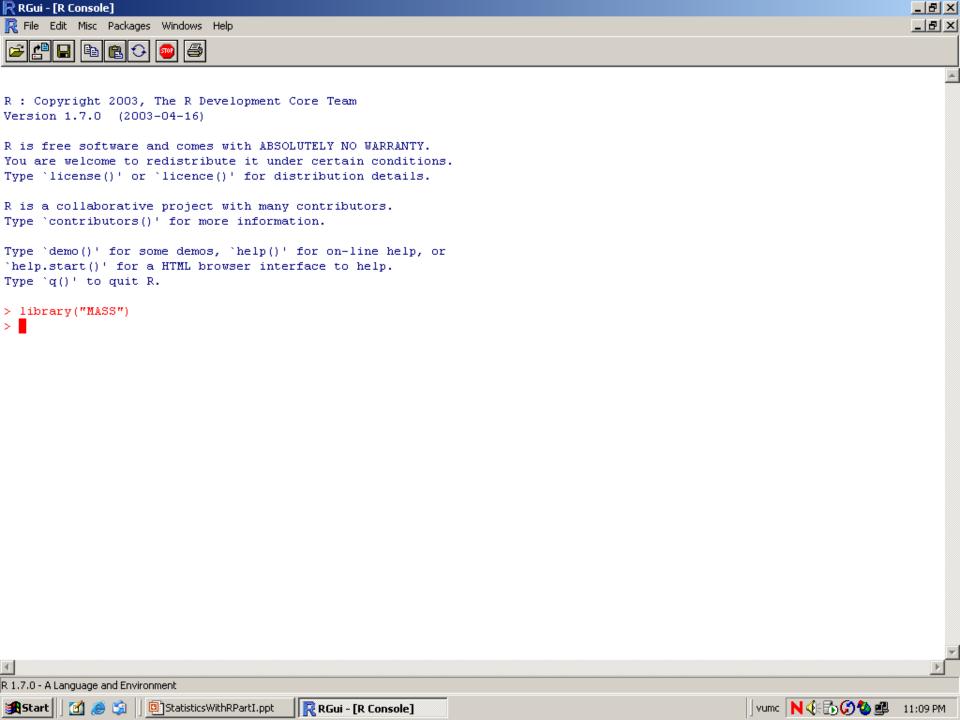
 State of the art: many statistical researchers provide their methods as R packages

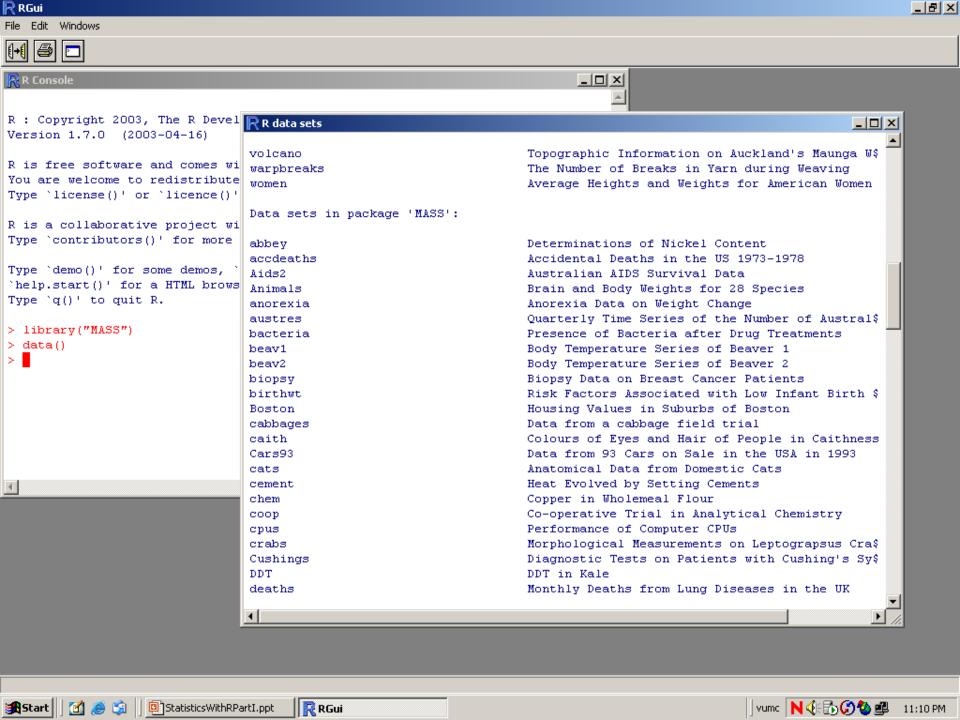
# History of R

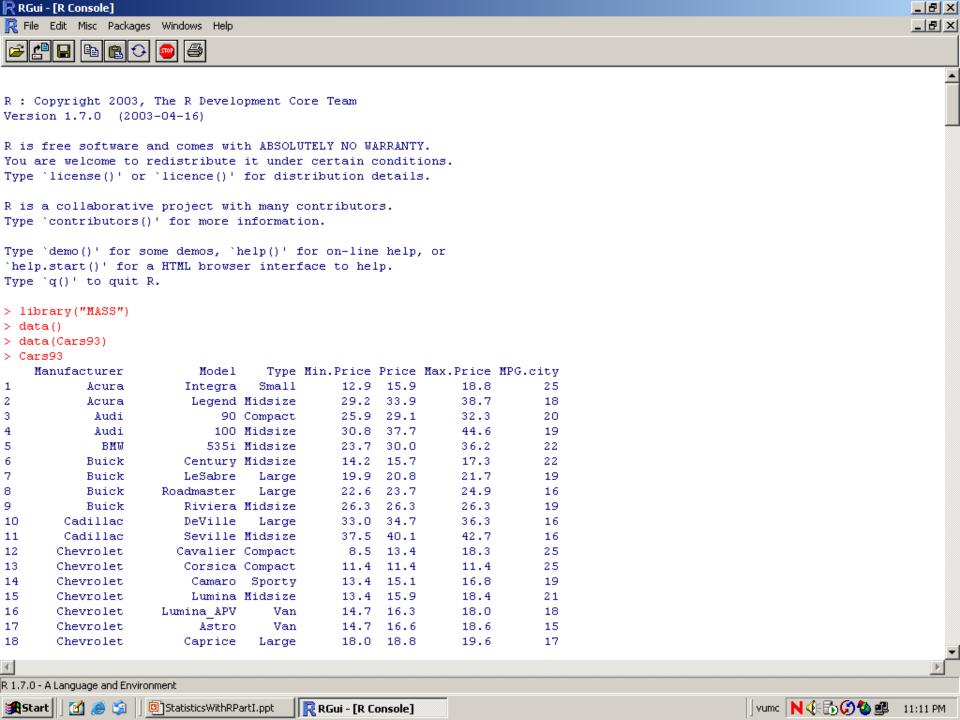
- Statistical programming language S developed at Bell Labs since 1976 (at the same time as UNIX)
- Intended to interactively support research and data analysis projects
- Exclusively licensed to Insightful ("S-Plus")
- R: Open source platform similar to S developed by R. Gentleman and R. Ihaka (U of Auckland, NZ) during the 1990s
- Since 1997: international "R-core" developing team
- Updated versions available every couple months

# Getting started

- To obtain and install R on your computer
  - Go to <a href="http://cran.r-project.org/mirrors.html">http://cran.r-project.org/mirrors.html</a> to choose a mirror near you
  - Click on your favorite operating system (Linux, Mac, or Windows)
  - Download and install the "base"
- To install additional packages
  - Start R on your computer
  - Choose the appropriate item from the "Packages" menu

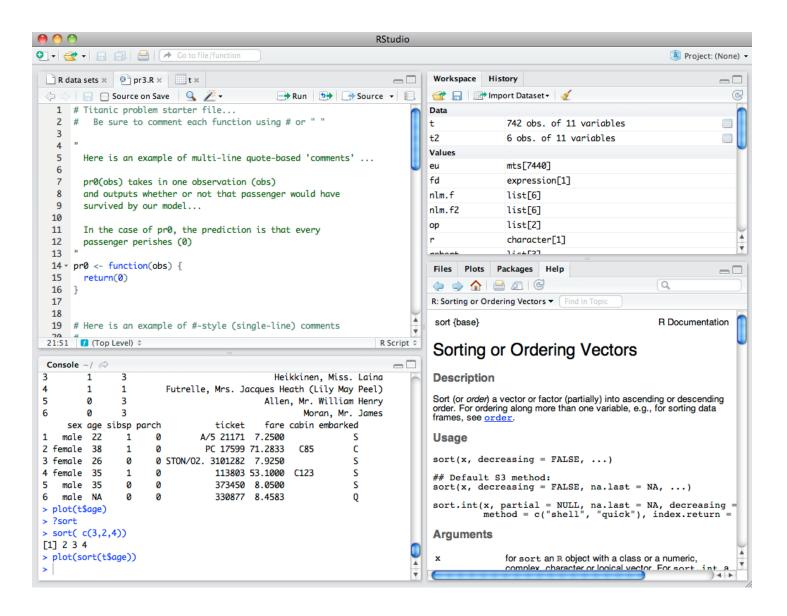






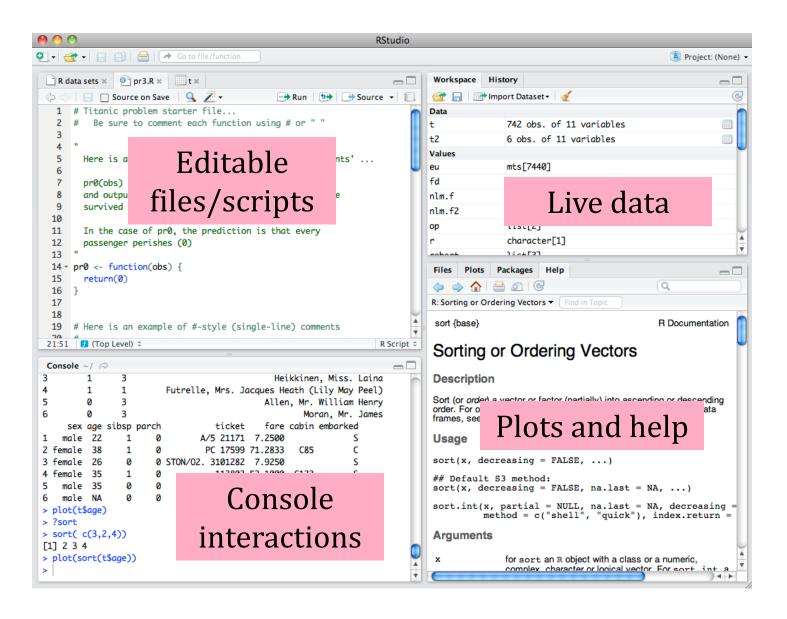
### **RStudio**

### An **IDE** that wraps R



### **RStudio**

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# Getting help... and quitting

- Getting information about a specific command
  - > help(rnorm)
  - > ?rnorm
- Finding functions related to a keyword
  - > help.search("boxplot")
- Starting the R installation help pages
  - > help.start()
- Quitting R
  - > q()

# Basic data types

# Objects

- variables = objects
- types of objects: vector, factor, array, matrix, data.frame, ts, list
- attributes
  - mode: integer, numeric, character, complex, logical
  - length: number of elements in object
- creation
  - assign a value
  - create a blank object

# Naming Convention

must start with a letter (A-Z or a-z)

- can contain letters, digits (0-9), and/or
  - periods "."
  - underscore " "

- case-sensitive
  - mydata different from MyData

# Assignment

• "<-" used to indicate assignment

```
x < -c(1, 2, 3, 4, 5, 6, 7)

x < -c(1:7)

x < -1:7
```

• note: as of version 1.4 "=" is also a valid assignment operator

### R as a calculator

```
> 5 + (6 + 7) * pi^2
[1] 133.3049
> log(exp(1))
[1] 1
> log(1000, 10)
[1] 3
> \sin(pi/3)^2 + \cos(pi/3)^2
\lceil 1 \rceil 1
> Sin(pi/3)^2 + cos(pi/3)^2
Error: couldn't find function "Sin"
```

### R as a calculator

```
> log2(32)
[1] 5
                                       \sin(\text{seq}(0, 2 * \text{pi}, \text{length} = 100))
> sqrt(2)
[1] 1.414214
> seq(0, 5, length=6)
[1] 0 1 2 3 4 5
                                                     20
                                                             40
                                                                            80
                                                                                    100
                                                                     60
                                                                Index
> plot(sin(seq(0, 2*pi, length=100)))
```

# Basic (atomic) data types

#### Logical

```
> x <- T; y <- F
> x; y
[1] TRUE
[1] FALSE
```

#### Numerical

```
> a <- 5; b <- sqrt(2)
> a; b
[1] 5
[1] 1.414214
```

#### Character

```
> a <- "1"; b <- 1
> a; b
[1] "1"
[1] 1
> a <- "character"</pre>
> b <- "a"; c <- a
> a; b; c
[1] "character"
[1] "a"
[1] "character"
```

# Data Type Conversion

- Type conversions in R work as you would expect. For example, adding a character string to a numeric vector converts all the elements in the vector to character.
- Use is. foo to test for data type foo. Returns TRUE or FALSE
   Use as. foo to explicitly convert it.
- is.numeric(), is.character(), is.vector(), is.matrix(), is.data.frame()
   as.numeric(), as.character(), as.vector(), as.matrix(), as.data.frame)

# Vectors, Matrices, Arrays

- Vector
  - Ordered collection of data of the same data type
  - Example:
    - last names of all students in this class
    - Mean intensities of all genes on an oligonucleotide microarray
  - In R, single number is a vector of length 1
- Matrix
  - Rectangular table of data of the same type
  - Example
    - Intensities of all genes measured during a microarray experiment
- Array
  - Higher dimensional matrix

### **Vectors**

 Vector: Ordered collection of data of the same data type

```
> x < -c(5.2, 1.7, 6.3)
> log(x)
[1] 1.6486586 0.5306283 1.8405496
> y <- 1:5
> z < - seq(1, 1.4, by = 0.1)
> y + z
[1] 2.0 3.1 4.2 5.3 6.4
> length(y)
[1] 5
> mean (y + z)
[1] 4.2
```

### **Vectors**

```
> Mydata <- c(2,3.5,-0.2) Vector (c="concatenate")
> Colors <-
   c ("Red", "Green", "Red") Character vector
> x1 < -25:30
> x1
                              Number sequences
[1] 25 26 27 28 29 30
> Colors[2]
                              One element (1-index!)
[1] "Green"
> x1[3:5]
                              Various elements
[1] 27 28 29
```

### Operation on vector elements

```
> Mydata
[1] 2 3.5 -0.2
> Mydata > 0

    Test on the elements

[1] TRUE TRUE FALSE
> Mydata[Mydata>0]

    Extract the positive elements

[1] 2 3.5
> Mydata[-c(1,3)]

    Remove elements

[1] 3.5
```

### Vector operations

```
> x < -c(5, -2, 3, -7)
> y < -c(1,2,3,4)*10
                                  Operation on all the elements
> y
[1] 10 20 30 40
> sort(x)
                                  Sorting a vector
[1] -7 -2 3 5
> order(x)
                                  Element order for sorting
[1] 4 2 3 1
> y[order(x)]
                                  Operation on all the components
[1] 40 20 30 10
                                  Reverse a vector
> rev(x)
[1] -7 3 -2 5
```

### Matrices

Matrix: Rectangular table of data of the same type

```
> m <- matrix(1:12, 4, byrow = T); m
      [,1] [,2] [,3]
[1,] 1 2
[2,] 4 5 6
[3,] 7 8 9
[4,] 10 11 12
> y <- -1:2
> m.new <- m + y
> t(m.new)
     [,1] [,2] [,3] [,4]
[1,] 0 4 8 12
[2,] 1 5 9 13
[3,] 2 6 10 14
> dim(m)
[1] 4 3
> dim(t(m.new))
[1] 3 4
```

### Matrices

Matrix: Rectangular table of data of the same type

```
> x < -c(3, -1, 2, 0, -3, 6)
> x.mat
    [,1] [,2]
[1,] 3 0
[2,] -1 -3
[3,] 2 6
> x.mat <- matrix(x,ncol=2,</pre>
                         By row creation
          byrow=T)
> x.mat
    [,1] [,2]
[1,] 3 -1
[2,] 2 0
[3,] -3 6
```

# Dealing with matrices

```
2<sup>nd</sup> col
> x.mat[,2]
[1] -1 0 6
                                  1<sup>st</sup> and 3<sup>rd</sup> lines
> x.mat[c(1,3),]
      [,1] [,2]
[1,] 3 -1
[2,] -3 6
                                  No 2<sup>nd</sup> line
> x.mat[-2,]
      [,1] [,2]
[1,] 3 -1
[2,] -3 6
```

# Dealing with matrices

> x.mat %\*% t(x.mat)

Multiplication

```
[,1] [,2] [,3]
[1,] 10 6 -15
[2,] 6 4 -6
[3,] -15 -6 45
```

- > solve () solves the equation A %\*% X = B for X,
- > eigen() Eigenvectors and eigenvalues

# Missing values

- R is designed to handle statistical data and therefore predestined to deal with missing values
- Numbers that are "not available"

```
> x <- c(1, 2, 3, NA)
> x + 3
[1] 4 5 6 NA
```

Testing for Missing Values

```
> is.na(x) # returns TRUE if x is missing
> y <- c(1,2,3,NA)
> is.na(y) # returns a vector (F F F T)
• "Not a number"
```

> log(c(0, 1, 2))
[1] -Inf 0.0000000 0.6931472
> 0/0
[1] NaN

# Missing values

- Excluding Missing Values from Analyses
  - Arithmetic functions on missing values yield missing values.

 The function complete.cases() returns a logical vector indicating which cases are complete.

```
# list rows of data that have missing values
> mydata[!complete.cases(mydata),]
```

 The function na.omit() returns the object with listwise deletion of missing values.

```
# create new dataset without missing data
> newdata <- na.omit(mydata)</pre>
```

# Subsetting

- It is often necessary to extract a subset of a vector or matrix
- R offers a couple of neat ways to do that

```
> x <- c("a", "b", "c", "d", "e", "f",
"g", "h")
> x[1]
> x[3:5]
> x[-(3:5)]
> x[c(T, F, T, F, T, F, T, F)]
> x[x <= "d"]
> m[,2]
> m[3,]
```

# Lists, data frames, and factors

### Lists

vector: an ordered collection of data of the same type.

```
> a = c(7,5,1)
> a[2]
[1] 5
```

list: an ordered collection of data of arbitrary types.

```
> doe = list(name="john",age=28,married=F)
> doe$name
[1] "john"
> doe$age
[1] 28
```

### Lists 1

- A list is an object consisting of objects called components.
- The components of a list don't need to be of the same mode or type and they can be a numeric vector, a logical value and a function and so on.
- A component of a list can be referred as aa [[i]] or aa\$times, where aa is the name of the list and times is a name of a component of aa.

## Lists 2

- The names of components may be abbreviated down to the minimum number of letters needed to identify them uniquely.
- aa[[1]] is the first component of aa, while aa[1] is the sublist consisting of the first component of aa only.
- There are functions whose return value is a List.

# Lists are very flexible

```
> \text{my.list} <- \text{list}(c(5,4,-1),c("X1","X2","X3"))
> my.list
[[1]]:
[1] 5 4 -1
[[2]]:
[1] "X1" "X2" "X3"
> my.list[[1]]
[1] 5 4 -1
> my.list <- list(c1=c(5,4,-1),c2=c("X1","X2","X3"))
> my.list$c2[2:3]
[1] "X2" "X3"
```

## Lists 3

```
Empl <- list(employee="Anna", spouse="Fred",
   children=3, child.ages=c(4,7,9))

Empl[[4]]

Empl$child.a

Empl[4]  # a sublist consisting of the 4th component of Empl
names(Empl) <- letters[1:4]

Empl <- c(Empl, service=8)

unlist(Empl)  # converts it to a vector. Mixed types will
be converted to character, giving a character vector.</pre>
```

## More lists

```
> x.mat
    [,1] [,2]
[1,] 3 -1
[2,] 2 0
[3,] -3 6
> dimnames(x.mat) <- list(c("L1","L2","L3"),</pre>
                         c("R1", "R2"))
> x.mat
   R1 R2
L1 3 -1
L2 2 0
L3 -3 6
```

## Data frames

data frame: represents a spreadsheet.

Rectangular table with rows and columns; data within each column has the same type (e.g. number, text, logical), but different columns may have different types.

#### Example:

```
> cw = chickwts
> CW
   weight
                feed
      179
                horsebean
11
     309
                linseed
23 243
                soybean
37
     423
                sunflower
```

### Data frames

#### Creating a data frame

```
> d <- c(1,2,3,4)
> e <- c("red", "white", "red", NA)
> f <- c(TRUE,TRUE,TRUE,FALSE)
> mydata <- data.frame(d,e,f)
> names(mydata) <- c("ID","Color","Passed")</pre>
```

#### Adding a new column

- > mydata\$Height <- c(100,120,120,130)
- > mydata\$Shape <- "circle"</pre>

# Subsetting

Individual elements of a vector, matrix, array or data frame are accessed with "[]" by specifying their index, or their name

```
> cw = chickwts
> CW
   weight
               feed
     179
               horsebean
11 309
               linseed
23 243
               soybean
37
  423
               sunflower
> cw [3,2]
[1] horsebean
6 Levels: casein horsebean linseed ... sunflower
> cw [3,]
 weight feed
    136 horsebean
```

# Subsetting

```
Other ways to subset...
# columns 3,4,5 of dataframe
> myframe[3:5]
# columns ID and Age from dataframe
> myframe[c("ID","Age")]
# variable ID in the dataframe
> myframe$ID
# using subset function
> subset( myframe, Age < 35, c("ID", "Age") )</pre>
```

# Merging

To merge two dataframes (datasets) horizontally, use the **merge** function. In most cases, you join two dataframes by one or more common key variables (i.e., an inner join).

# Merging

#### **ADDING ROWS**

To join two dataframes (datasets) vertically, use the **rbind** function. The two dataframes **must** have the same variables, but they do not have to be in the same order.

```
total <- rbind(dataframeA, dataframeB)</pre>
```

If dataframeA has variables that dataframeB does not, then either:

- Delete the extra variables in dataframeA or
- Create the additional variables in dataframeB and <u>set them to NA</u> (missing) before joining them with rbind.

# Aggregating

- It is relatively easy to collapse data in R using one or more BY variables and a defined function.
- # aggregate dataframe mtcars by cyl, returning means for numeric variables

## **Factors**

Tell **R** that a variable is **nominal** by making it a factor. The factor stores the nominal values as a vector of integers in the range [ 1... k ] (where k is the number of unique values in the nominal variable), and an internal vector of character strings (the original values) mapped to these integers.

```
variable gender with 20 "male" entries and 30 "female" entries
    gender <- c(rep("male", 20), rep("female", 30))
    gender <- factor(gender)

stores gender as 20 1s and 30 2s and associates

1=female, 2=male internally (alphabetically)

R now treats gender as a nominal variable
    summary (gender)</pre>
```

# Control structures

#### Control Structures

Control structures in R allow you to control the flow of execution of the program, depending on runtime conditions. Common structures are

- if, else: testing a condition
- for: execute a loop a fixed number of times
- while: execute a loop while a condition is true
- repeat: execute an infinite loop
- break: break the execution of a loop
- next: skip an interation of a loop
- return: exit a function

Most control structures are not used in interactive sessions, but rather when writing functions or longer expresisons.

#### Control Structures: if

```
if(<condition>) {
        ## do something
} else {
        ## do something else
}
if(<condition1>) {
        ## do something
} else if(<condition2>) {
        ## do something different
} else {
        ## do something different
```

This is a valid if/else structure.

```
if(x > 3) {
          y <- 10
} else {
          y <- 0
}</pre>
```

So is this one.

```
y <- if(x > 3) {
          10
} else {
          0
}
```

```
if(x > 1) {
        print("x is big")
} else if(x > 0) {
        print("x is positive")
} else {
        print("x is negative or zero")
```

How are these two conditionals different?

```
if(x > 1) {
          print("x is big")
}
if(x > 0) {
          print("x is positive")
}
print("x is negative or zero")
```

for loops take an interator variable and assign it successive values from a sequence or vector. For loops are most commonly used for iterating over the elements of an object (list, vector, etc.)

```
for(i in 1:10) {
          print(i)
}
```

This loop takes the i variable and in each iteration of the loop gives it values 1, 2, 3, ..., 10, and then exits.

```
These three loops have the same behavior.
x <- c("a", "b", "c", "d")
for(i in 1:4) {
        print(x[i])
for(i in seq_along(x)) {
        print(x[i])
for(letter in x) {
        print(letter)
}
for(i in 1:4) print(x[i])
```

seq\_along creates
a list of indices

#### while

While loops begin by testing a condition. If it is true, then they execute the loop body. Once the loop body is executed, the condition is tested again, and so forth.

```
count <- 0
while(count < 10) {
    print(count)
    count <- count + 1
}</pre>
```

While loops can potentially result in infinite loops if not written properly. Use with care!

#### while

Sometimes there will be more than one condition in the test.

```
z <- 5
while(z \ge 3 \&\& z \le 10) {
        print(z)
        coin \leftarrow rbinom(1, 1, 0.5)
        if(coin == 1) { ## random walk
                 z < -z + 1
        } else {
                 z < -z - 1
```

Conditions are always evaluated from left to right.

#### repeat

Repeat initiates an infinite loop; these are not commonly used in statistical applications but they do have their uses. The only way to exit a repeat loop is to call break.

```
x0 <- 1
tol <- 1e-8

repeat {
          x1 <- computeEstimate()

          if(abs(x1 - x0) < tol) {
                break
          } else {
                x0 <- x1
          }
}</pre>
```



#### next, return

# Arithmetic Operators

Operator	Description
+	addition
-	subtraction
*	multiplication
1	division
^ or **	exponentiation
x %% y	modulus (x mod y) 5%%2 is 1
x %/0/% y	integer division 5%/%2 is 2

## Arithmetic Operators

## Vector functions

```
> \text{vec} < - c(5,4,6,11,14,19)
> sum(vec)
[1] 59
                            And also: min() max()
> prod(vec)
                                  cummin() cummax()
[1] 351120
                                  cumsum()
                                             cumprod()
> mean (vec)
                                  range()
[1] 9.833333
> median(vec)
[1] 8.5
> var(vec)
[1] 34.96667
> sd(vec)
[1] 5.913262
> summary(vec)
   Min. 1st Qu.
                 Median
                            Mean 3rd Qu.
                                              Max.
  4.000
          5.250
                   8.500
                            9.833 13.250 19.000
```

# Logical Operators

Operator	Description
<	less than
<=	less than or equal to
>	greater than
>=	greater than or equal to
==	exactly equal to
!=	not equal to
!x	Not x
$\mathbf{x} \mid \mathbf{y}$	x OR y
x & y	x AND y
isTRUE(x)	test if x is TRUE

## Statistical functions

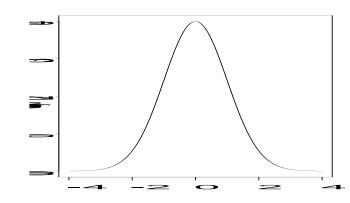
Normal distr

$$f(x \mid \mu, \sigma) = \frac{1}{\sigma \sqrt{2\pi}} e^{-\frac{1}{2} \left(\frac{x-\mu}{\sigma}\right)^2}$$

> dnorm(2,mean=1,sd=2)

[1] 0.1760327

PDF in point 2 for  $X \sim N(1,4)$ 



> qnorm(0.975)

[1] 1.959964

Quantile for

the 0.975 for  $N \sim (0,1)$ 

- > pnorm(c(2,3),mean=2)
- = P(X<2) and P(X<3), where  $X \sim N(2,1)$
- [1] 0.5000000 0.8413447
- > norm.alea <- rnorm(1000) Pseudo-random normally distributed numbers
- > summary(norm.alea)

Min. 1st Qu. Median Mean 3rd Qu. Max.

- -3.418 -0.6625 -0.0429 -0.01797 0.6377 3.153
- > sd(norm.alea)
- 1] 0.9881418

## How to remember functions

For a normal distribution, the root is **norm**. Then add the letters

```
d density (dnorm())
p probability(pnorm())
q quantiles (qnorm())
r pseudo-random (rnorm())
```

Distribution	Root	Argument
normal	norm	mean, sd, log
t (Student)	t	df, log
uniform	unif	min, max, log
F (Fisher)	f	df1, df2
χ2	chisq	df, ncp, log
Binomial	binom	size, prob, log
exponential	exp	rate, log
Poisson	pois	lambda, log

• • •

Function	Description
dnorm(x)	normal density function (by default m=0 sd=1) # plot standard normal curve x <- pretty(c(-3,3), 30) y <- dnorm(x) plot(x, y, type='l', xlab="Normal Deviate", ylab="Density", yaxs="i")
$\mathbf{pnorm}(q)$	cumulative normal probability for q (area under the normal curve to the right of q) pnorm(1.96) is 0.975
qnorm(p)	normal quantile. value at the p percentile of normal distribution qnorm(.9) is 1.28 # 90th percentile
<b>rnorm</b> ( <i>n</i> , <b>m</b> =0, <b>sd</b> =1)	n random normal deviates with mean m and standard deviation sd. #50 random normal variates with mean=50, sd=10 x <- rnorm(50, m=50, sd=10)
<b>dbinom</b> (x, size, prob) <b>pbinom</b> (q, size, prob) <b>qbinom</b> (p, size, prob) <b>rbinom</b> (n, size, prob)	binomial distribution where size is the sample size and prob is the probability of a heads (pi) # prob of 0 to 5 heads of fair coin out of 10 flips dbinom(0:5, 10, .5) # prob of 5 or less heads of fair coin out of 10 flips pbinom(5, 10, .5)
<pre>dpois(x, lamda) ppois(q, lamda) qpois(p, lamda) rpois(n, lamda)</pre>	poisson distribution with m=std=lamda #probability of 0,1, or 2 events with lamda=4 dpois(0:2, 4) # probability of at least 3 events with lamda=4 1- ppois(2,4)
<pre>dunif(x, min=0, max=1) punif(q, min=0, max=1) qunif(p, min=0, max=1) runif(n, min=0, max=1)</pre>	uniform distribution, follows the same pattern as the normal distribution above. #10 uniform random variates x <- runif(10)

# Importing/ Exporting Data

# Importing/Exporting Data

- Importing data
  - R can import data from other applications
  - Packages are available to import microarray data, Excel spreadsheets etc.
  - The easiest way is to import tab delimited files

```
> SimpleData <- read.table(
file = "http://eh3.uc.edu/SimpleData.txt",
header = TRUE,
quote = "",
sep = "\t",
comment.char="")</pre>
```

- Exporting data
  - R can also export data in various formats
  - Tab delimited is the most common

```
> write.table(x, "filename") *)
```

\*) make sure to include the path or to first change the working directory

## Credits

- Roger D. Peng
- Gilberto Câmara (R a brief introduction)
- Ralitza Gueorguieva (R Basics)